

Figure 1.

```
Sequence type explicitly set to Protein
Sequence format is Pearson
Sequence 1: new_S100_cytokine      104 aa
Sequence 2: G491246                110 aa
Sequence 3: W27152                 98 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 23
Sequences (1:3) Aligned. Score: 34
Sequences (2:3) Aligned. Score: 29
Start of Multiple Alignment
There are 2 groups
Aligning...
Group 1:                          Delayed
Group 2:                          Delayed
Sequence:1      Score:0
Sequence:3      Score:839
Sequence:2      Score:724
Alignment Score 444
CLUSTAL-Alignment file created [/data4/genetools/lrastelli4630clustalw]
```

Multiple Alignment:

```
new_S100_cytokine MGQCRSANAEDAQEFSDVERAIETLIKNFHQYSVEGG-KETLTTPSELRLVTQQLPHLMP
W27152            -----MAAEPSTLELES IETVITTFTEARQEGRKDSL SVNEFKELVTQQLPHLLK
G491246           -----MSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLK

new_S100_cytokine SNCG----LEEKIKANLQSCNDSKLEFRSEFWELIGEAAKSVKLERP---VRSH-----
W27152            DVGS----LDEKMKSLDVNQDSSELKNEYWRLLIGELAKEIRKKKD---EKIRKK-----
G491246           KENKNEKVFEHIMEDLDINADKQLSFEFI MLMARLTWASHEKMHGDEGP SHHHPGLG

new_S100_cytokine ---- (15-118 of SEQ ID NO:6)
W27152            ---- (SEQ ID NO: 10)
G491246           EGTP (SEQ ID NO:11)
```

Alignments Done: 535470

Mouse-over to show defline and score. Click to show alignments

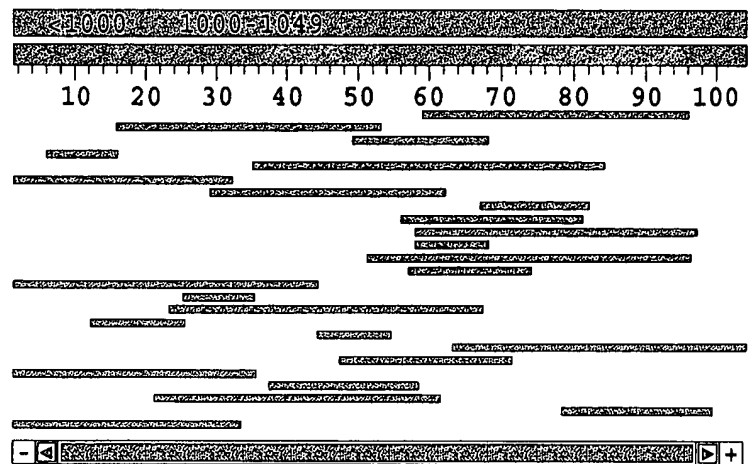


Fig. 4A

AC#	Description	Strength	Score	RF	AA#
BL00303B	0 3-100/ICaBP type calcium binding protein.	1336	1057	0	59 sNCGLEEKI aNLgScnDSLeFRSfWELIGeAAKsVrk (SEQ ID NO:12)
BL00303A	0 3-100/ICaBP type calcium binding protein.	1345	1038	0	16 DVERAIEtLIkNFhQYsVgGkEtltpSELrdlvtQQ (SEQ ID NO:13)
BL00874A	0 Bacterial type II secretion system protein F	1456	1021	0	49 VTQQLpHLmPsnCgLEEKI (SEQ ID NO:14)
BL00972B	0 Ubiquitin carboxyl-terminal hydrolases family	1227	991	0	6 AnaEAQqFFs (SEQ ID NO:15)
BL00538G	0 Bacterial themotaxis sensory transducers prot	1758	990	0	35 GgKEtLtpseLRdlVTQQLpHLmPsnCgLEEKIaNLgscnDSkLEFRsf (SEQ ID NO:16)
BL00532I	0 Phosphoenolpyruvate carboxykinase (ATP) prote	1412	989	0	0 mgQcRSAnAeAQefSdVErAIEtLIkNFhQY (SEQ ID NO:17)
BL00704A	0 Prokaryotic-type carbonic anhydrases proteins	1539	987	0	29 hqYsvegGketLtpseLRdlVTQQLpHLmPsnC (SEQ ID NO:18)
BL01017E	0 Ergosterol biosynthesis ERG4/ERG24 family pro	1499	983	0	67 ianlgScnDSkLEFR (SEQ ID NO:19)
BL00310E	0 Lysosome-associated membrane glycoproteins du	1633	976	0	56 lMpSncgLEEKIaNLgScnDSkLEf (SEQ ID NO:20)
BL00433C	0 Phosphofructokinase proteins.	1581	976	0	58 pSncGLEEKIaNLgScnDSkLEfRsfuELIGeAAKsVKI (SEQ ID NO:21)
BL50003	0 PH domain proteins profile.	990	976	0	58 PSNCGLEEKI (SEQ ID NO:22)
BL00459	0 Hyotoxins proteins.	2173	974	0	51 qqlpKlmpsnCgLEEKIaNLgScnDSkLEfRsfWELIGeAAKsVKI (SEQ ID NO:23)
BL50007C	0 Phosphatidylinositol-specific phospholipase X	1433	974	0	57 mPsnCgLEEKIaNLgSc (SEQ ID NO:24)
BL01207B	0 Glypicans proteins.	1508	973	0	-1 mggCrSaNAEDaQeFsDVErAIEtLIkNFhQYsvegGketLtpSE (SEQ ID NO:25)
BL00279B	0 Membrane attack complex components / perforin	1127	972	0	25 iKNFhQYsVE (SEQ ID NO:26)
BL01120D	0 Urease nickel ligands proteins.	1692	970	0	23 TLkNFhQYsvegGketLtpSELRdlvtQQpHLmPsnCgLEEK (SEQ ID NO:27)
BL00175B	0 Phosphoglycerate mutase family phosphohistidi	1298	968	0	12 qeFSDErAIEtL (SEQ ID NO:28)
BL00579A	0 Ribosomal protein L23 proteins.	1092	967	0	44 ELRDLVTQQL (SEQ ID NO:29)
BL00832B	0 2'-5'-oligoadenylate synthetases proteins.	1826	967	0	63 LeekiaNLgScnDSkLEfRsfWELIGeAAKsVKLEFrVrgh (SEQ ID NO:30)
BL01005C	0 Formate and nitrite transporters proteins.	1552	964	0	47 dLVtqQLpHLmPsnCgLEEKIaNL (SEQ ID NO:31)
BL00261A	0 Glycoprotein hormones beta chain proteins.	1528	963	0	1 qQCRsANAedaqEFsDVErAIEtLIkNFhQYsVE (SEQ ID NO:32)
BL00663A	0 Vinculin family talin-binding region proteins	1567	963	0	37 keTLtpseLRdlVTQQLpKln (SEQ ID NO:33)
BL00743A	0 Beta-lactamases class B proteins.	1580	960	0	21 IeTLkNFhQYsvegGketLtpseLRdlVTQQLpHLmPsn (SEQ ID NO:34)
BL01031B	0 Heat shock hsp20 proteins family profile.	1200	960	0	78 LEFRSFWELIGeAAKsVKLEFR (SEQ ID NO:35)
BL01062C	0 Hydroxymethylglutaryl-coenzyme A lyase protei	1908	960	0	-2 MggrCsAnAeAQefSdVErAIEtLIkNFhQYsVE (SEQ ID NO:36)

Fig. 4A (Continued)

Figure 7

*****Contig 1*****									
	.	:	.	:	.	:	.	:	.
65677221+	GAATTCAGAGGAGTTCTCAGTGCCCCGGACAGGCCCTCTCCAGCTTCACACTCTTGGC								
AA315020-	TGCCCCCGGACAGTCCCTCTCNAGCTTCACACTCTTGGC								
consensus	GAATTCAGAGGAGTTCTCAGTGCCCCGGACAGGCCCTCTCCAGCTTCACACTCTTGGC								
	.	:	.	:	.	:	.	:	.
65677221+	CGCTTCTCCAATCAGCTCCAGAAACTCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
AA315020-	CGCTTCTCCAATCAGCTCCAGAAACTCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
consensus	CGCTTCTCCAATCAGCTCCAGAAACTCTGAACTCCAGTTTAGAGTCATTGCAGCTGCC								
	.	:	.	:	.	:	.	:	.
65677221+	CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCAGCTGTG								
AA315020-	CAGGTTGGCAATTTTCTCTTCCAGGCCANAGTTGCTCGGCATGAGATGGGGCAGCTGTG								
consensus	CAGGTTGGCAATTTTCTCTTCCAGGCCACAGTTGCTCGGCATGAGATGGGGCAGCTGTG								
	.	:	.	:	.	:	.	:	.
65677221+	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTGACGGTCTCCTTCCCACCCCTCCACGGAGTA								
AA315020-	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTGACGGTCTCCTTCCCACCCCTCCACGGAGTA								
consensus	GGTGACCAAGGTCCCGTAGCTCAGAAGGGGTGACGGTCTCCTTCCCACCCCTCCACGGAGTA								
	.	:	.	:	.	:	.	:	.
65677221+	CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTC (SEQ ID NO: 37)								
AA315020-	CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC								
consensus	CTGGTGAAAGTTCTTGATGAGGGTCTCAATGGCCCTCTCCACATCACTGAATTCCTGAGC								
	.	:	.	:	.	:	.	:	.
AA315020-	ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGTCTACTGTGTGGTCCCTTGGT								
consensus	ATCCTCTGCGTTGGCTGACCGACACTGTCCCATGGTGTCTACTGTGTGGTCCCTTGGT								
	.	:	.	:	.	:	.	:	.
AA315020-	GAGAGTTCTGTGTCCCTAT (SEQ ID NO: 48)								
consensus	GAGAGTTCTGTGTCCCTAT (SEQ ID NO: 5)								